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B. Bonner

#16

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RAW SEQUENCE LISTING              DATE: 08/27/2002
PATENT APPLICATION:  US/09/721,341   TIME: 10:54:51

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         Output Set: N:\CRF4\08272002\I721341.raw
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ENTERED

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 3 <110> APPLICANT: Gosling, Jennifa
 4        Dairaghi, Daniel J.
 5        Hanley, Michael
 6        Miao, Zhenhua
 7        Schall, Thomas J.
 8        ChemoCentryx, Inc.
10 <120> TITLE OF INVENTION: Chemokine Receptor
12 <130> FILE REFERENCE: 019934-000710US
14 <140> CURRENT APPLICATION NUMBER: 09/721,341
15 <141> CURRENT FILING DATE: 2000-11-21
17 <150> PRIOR APPLICATION NUMBER: US 09/686,020
18 <151> PRIOR FILING DATE: 2000-10-10
20 <150> PRIOR APPLICATION NUMBER: US 60/159,015
21 <151> PRIOR FILING DATE: 1999-10-12
23 <150> PRIOR APPLICATION NUMBER: US 60/159,210
24 <151> PRIOR FILING DATE: 1999-10-13
26 <150> PRIOR APPLICATION NUMBER: US 60/172,979
27 <151> PRIOR FILING DATE: 1999-12-20
29 <150> PRIOR APPLICATION NUMBER: US 60/173,388
30 <151> PRIOR FILING DATE: 1999-12-28
32 <150> PRIOR APPLICATION NUMBER: US 60/186,626
33 <151> PRIOR FILING DATE: 2000-03-03
35 <160> NUMBER OF SEQ ID NOS: 14
37 <170> SOFTWARE: PatentIn Ver. 2.1
39 <210> SEQ ID NO: 1
40 <211> LENGTH: 1147
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
44 <220> FEATURE:
45 <221> NAME/KEY: CDS
46 <222> LOCATION: (1)..(1053)
48 <220> FEATURE:
49 <223> OTHER INFORMATION: chemokine receptor (CCX CKR)
51 <400> SEQUENCE: 1
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53 Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
54   1           5               10              15
56 gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc   96
57 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
58           20              25              30
60 aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc  144
61 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
62      35              40                  45
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66  aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca    192
67  Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
68      50                      55                      60
70  att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc    240
71  Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
72  65                      70                      75                      80
74  ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt    288
75  Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
76                  85                      90                      95
78  tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc    336
79  Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
80              100                     105                     110
82  aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag    384
83  Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
84          115                     120                     125
86  ttt ctg gct tgt atc agc ata gac aga tat gtg gca gta act aaa gtc    432
87  Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
88      130                     135                     140
90  ccc agc caa tca gga gtg gga aaa cca tgc tgg atc atc tgt ttc tgt    480
91  Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
92  145                     150                     155                     160
94  gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat    528
95  Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
96              165                     170                     175
98  aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta    576
99  Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
100             180                     185                     190
102 gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga    624
103 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
104         195                     200                     205
106 ttt gta gta ccc ttt ctt att atg ggg gtg tgc tac ttt atc aca gca    672
107 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
108     210                     215                     220
110 agg aca ctc atg aag atg cca aac att aaa ata tct cga ccc cta aaa    720
111 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
112 225                     230                     235                     240
114 gtt ctg ctc aca gtc gtt ata gtt ttc att gtc act caa ctg cct tat    768
115 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
116             245                     250                     255
118 aac att gtc aag ttc tgc cga gcc ata gac atc atc tac tcc ctg atc    816
119 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
120         260                     265                     270
122 acc agc tgc aac atg agc aaa cgc atg gac atc gcc atc caa gtc aca    864
123 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
124     275                     280                     285
128 gaa agc atc gca ctc ttt cac agc tgc ctc aac cca atc ctt tat gtt    912
129 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
130     290                     295                     300
132 ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa    960
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133 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
134 305              310              315              320
136 tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt   1008
137 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
138              325              330              335
140 gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa       1053
141 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
142              340              345              350
144 aggtaaaact gctctgcctt ttgcttggat acatatgaat gatgctttcc cctcaaataa 1113
146 aacatctgcc ttattctgaa aaaaaaaaaa aaam                              1147

149 <210> SEQ ID NO: 2
150 <211> LENGTH: 350
151 <212> TYPE: PRT
152 <213> ORGANISM: Homo sapiens
153 <220> FEATURE:
154 <223> OTHER INFORMATION: chemokine receptor (CCX CKR)
156 <400> SEQUENCE: 2
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158   1               5              10              15
159 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
160              20              25              30
161 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
162              35              40              45
163 Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
164        50              55              60
165 Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
166   65              70              75              80
167 Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
168              85              90              95
169 Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
170              100             105             110
171 Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
172        115             120             125
173 Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
174        130             135             140
175 Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
176 145             150             155             160
177 Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
178              165             170             175
179 Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
180              180             185             190
181 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
182        195             200             205
183 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
184        210             215             220
185 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
186 225             230             235             240
187 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
188              245             250             255
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Input Set : N:\Crf3\RULE60\09721341.txt
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191 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
192             260             265             270
193 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
194             275             280             285
195 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
196         290             295             300
197 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
198 305                 310             315                 320
199 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
200             325             330                 335
201 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
202             340             345             350
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 1147
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
211 <220> FEATURE:
212 <223> OTHER INFORMATION: chemokine receptor (variant)
214 <400> SEQUENCE: 3
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216 actgatgact acagtcagta tgaactgatc tgtatcaaag aagatgtcag agaatttgcc  120
217 aaagtttttcc cccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc  180
218 atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc  240
219 ctgaatttgg ctgtagcaga tttactcctt ctattcactc tgccttttttg ggctgttaat  300
220 gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca  360
221 ctaaactttg tctctggaat gcagtttctg cttgtatca gcatagacag atatgtggca  420
222 gtaactaaag tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt  480
223 gtctggatgg ctgccatctt gctgagcata ccccagctgg tttttttatac agtaaatgac  540
224 aatgttaggt gcattcccat tttccccgc aacttaggaa catcaatgaa agcattgatt  600
225 caaatgctag agatctgcat tggatttgta gtacccttctc ttattatggg ggtgtgctac  660
226 tttatcacag caaggacact catgaagatg ccaaacatta aaatatctcg accccctaaaa  720
227 gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag  780
228 ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc  840
229 atggacatcg ccatccaagt cacagaaagc atcgcactct ttcacagctg cctcaaccca  900
230 atcctttatg tttttatggg agcatctttc aaaaactacg ttatgaaagt ggccaagaaa  960
231 tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggt 1020
232 cctacagagc caaccagtac ttttagcatt taaaggtaaa actgctctgc cttttgcttg 1080
233 gatacatatg aatgatgctt cccctcaaa taaaacatct gccttattct gaaaaaaaaa 1140
234 aaaaaam                                                         1147
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238 <211> LENGTH: 25
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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252 <211> LENGTH: 19
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254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
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265 <212> TYPE: PRT
266 <213> ORGANISM: Homo sapiens
268 <220> FEATURE:
269 <223> OTHER INFORMATION: chemokine receptor (CCR9)
271 <400> SEQUENCE: 6
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278 Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln Phe Ala Ser
279         35                  40                  45
281 His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val Gly Ala Leu
282     50                  55                  60
284 Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr Arg Val Lys
285 65                  70                  75                  80
287 Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala Asp Leu Leu
288             85                  90                  95
290 Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala Asp Gln Trp
291             100                 105                 110
293 Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met Tyr Lys Met
294         115                 120                 125
296 Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser Val Asp Arg
297     130                 135                 140
299 Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp Arg Glu Lys
300 145                 150                 155                 160
302 Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp Val Leu Ala
303             165                 170                 175
305 Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile Lys Glu Glu
306             180                 185                 190
308 Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp Glu Ser Thr
309         195                 200                 205
313 Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu Gly Phe Phe
314     210                 215                 220
316 Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile Ile His Thr
317 225                 230                 235                 240
319 Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu Lys Val Thr
320             245                 250                 255
322 Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro Tyr Asn Cys
323             260                 265                 270
325 Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe Ile Ser Asn
326         275                 280                 285
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Input Set : N:\Crf3\RULE60\09721341.txt
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